



EXHIBIT 1

Alignment of SEQ ID NO:1 (10/609,150) and SEQ ID NO:5 (Schweighoffer)

Score = 404 bits (210), Expect = 4e-109

Identities = 612/813 (75%), Gaps = 0/813 [Note- alignment across the entire Schweighoffer sequence gives an alignment of 612/865= 71% homology]

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SEQ5  52      CATAATATTACATTTTCAGAGTTCACCTCCCACAGTTGAGTGGCATATAAGCAGACCTGGG 111
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
SEQ1  2242     CATAATATTACCTTTGAAAGTCCACCTCCACCAATTGAATGGCATATCAGCAAACCAGGA 2301

Query   112     CACATAGAGACTTTTGACCTGCTCACCTTACACCCAATAGAAATTGCTCGACAACCTCACT 171
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2302     CAGTTTGAAACATTTGATCTCATGACACTTGATCCAATAGAAATTGCACGTGAGCTGACA 2361

Query   172     TTACTTGATTGAGATCTATACCGAGCTGTACAGCCATCAGATTTAGTTGGAAGTGTGTGG 231
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2362     CTTTGGAGTCTGATCTTTACAGGAAAGTTCAACCGTCTGAACCTGTAGGGAGTGTGTGG 2421

Query   232     ACAAAGAAGACAAAGAAATTAAGTCTCCTAATCTTCTGAAAATGATTGACATACCACC 291
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2422     ACCAAAGAAGATAAAGAAATAAATTCTCCAAATTTATTAAAAATGATTGCGCATACCACA 2481

Query   292     AACCTCACTCTGTGGTTTGAGAAATGTATTGTAGAAACTGAAAATTTAGAAGAAAGAGTA 351
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2482     AATCTCACCTCTGGTTTGAAAAATGCATTGTGGAAGCAGAAAATTTTGAAGAACGGGTG 2541

Query   352     GCTGTGGTGAGTCGAATTATTGAGATTCTACAAGTCTTTCAAGAGTTGAACAACCTTTAAT 411
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2542     GCAGTACTAAGTAGAATTATAGAAATCTGCAAGTTTTTCAAGATTGAATAATTTCAAT 2601

Query   412     GGGGTCCTTGAGGTTGTGAGTGCTATGAATTCCTCACCTGTTTACAGACTAGACCACACA 471
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2602     GGCGTATTGGAGATAGTCAGTGCAAGTAAATTCAGTGTCAGTATACAGACTAGACCATACC 2661

Query   472     TTTGAGCAAATACCAAGTCGCCAGAAGAAAATTTTAGAAGAAGCTCATGAATTGAGTGAA 531
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2662     TTTGAGGCACTGCAGGAAAGGAAAAGGAAAATTTTGACGAAGCTGTGGAATTAAGTCAA 2721

Query   532     GATCACTATAAGAAATATTTGGCAAAACTCAGGTCTATTAATCCACCATGTGTGCCTTTC 591
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2722     GATCACTTTAAAAAATACCTAGTAAACTTAAGTCAATCAATCCACCTTGTGTGCCTTTT 2781

Query   592     TTTGGAATTTATCTACATAATATCTTGAAACAGAAGAAGGCAACCCTGAGGTCTTAAAA 651
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2782     TTTGGAATATATTTAACAAATATTCTGAAGACCGAAGAAGGGAATAATGATTTTTTAAAA 2841

Query   652     AGACATGGAAAAGAGCTTATAAACTTTAGCAAAAGGAGGAAAGTAGCAGAAATAACAGGA 711
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2842     AGAAAGGGAAAAGATTTAATCAATTTAGTAAGAGGAGGAAAGTAGCTGAAATTACTGGA 2901

Query   712     GAGATCCAGCAGTACCAAAATCAGCCTTACTGTTTACGAGTAGAATCAGATATCAAAGG 771
      || || || || || || || || || || || || || || || || || || || || ||
Sbjct   2902     GAAATTCAGCAGTATCAGAATCAGCCTTACTGTTTACGGATAGAACAGATATGAGGAGA 2961

Query   772     TTCTTTGAAAACCTGAATCCGATGGGAAATAGCATGGAGAGGGAATTTACAGATTATCTT 831
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Sbjct 2962 TTCTTTGAAAACCTTAACCCCATGGGAAGTGCATCTGAAAAAGAGTTTACAGATTATTG 3021

Query 832 TTCAACAAATCCCTAGAAATAGAACCACGAAAC 864

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Sbjct 3022 TTCAACAAGTCACTAGAAATTGAACCTCGAAAC 3054

Alignment of 10/609,150 SEQ ID NO:2 with SEQ ID NO:1:

Score = 48.8 bits (25), Expect = 2e-04
Identities = 25/25 (100%), Gaps = 0/25 (0%)
Strand=Plus/Minus

Query 1 GAGGGTGAGATTTGTGGTATGGCGA 25
||||||| ||||||| ||||||| |||||
Sbjct 2493 GAGGGTGAGATTTGTGGTATGGCGA 2469

Alignment of 10/609,150 SEQ ID NO:3 with SEQ ID NO:1:

Score = 48.8 bits (25), Expect = 2e-04
Identities = 25/25 (100%), Gaps = 0/25 (0%)
Strand=Plus/Minus

Query 1 TGAGGAAAGGTCTTCTGAACTCGCT 25
||||||| ||||||| ||||||| |||||
Sbjct 239 TGAGGAAAGGTCTTCTGAACTCGCT 215